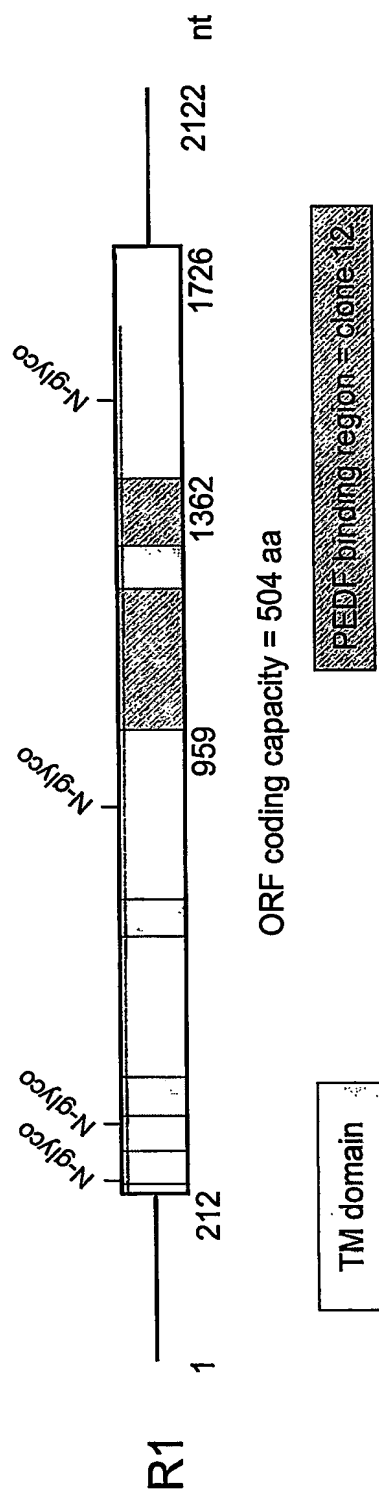
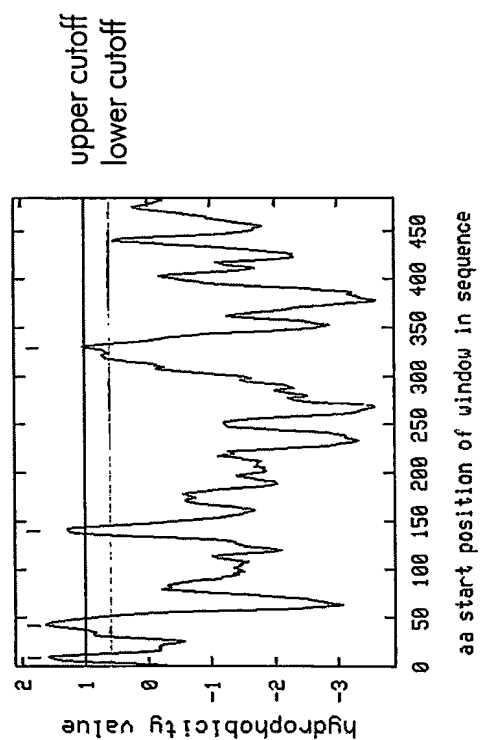


**Figure 1.**

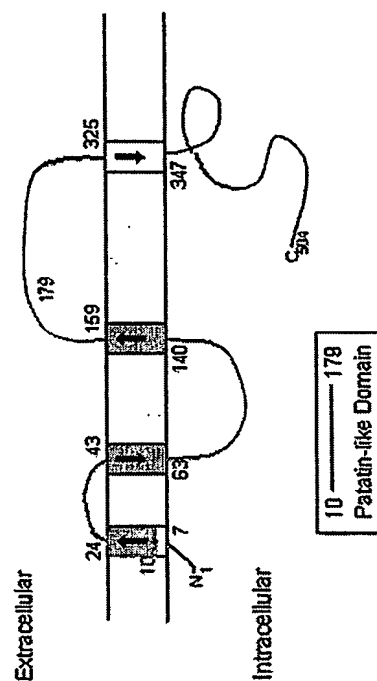
**A.**



**മ്**



○



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Figure 1.  
D.

R1  
adiponutrin

MFPREKTNWISFAGCGFLGVYVGVASCLREHAPFLVANATHIYGASAGALTATALTGTGVCCLGEAGAKFIEVSKEARKRFLG  
YDA RG SL F H ATR H LRD RMLF HCVGVLS I P EQTLQVLSDLVRK S NI

PLHPSFNLVKIIRSFLLKVLPA DSHEHASGRLGISLTRVSDGENVIISHFNKDELIAQNVCSGFIPIVYCGLIIPPSLQGVRYV  
IF S FL QG C C NV QLI KI LV DFR VVD L C F S FR

DGGISDNLPLYELKNTITVSPFSGESDIPQDSSTNIHELRTVNTSIQFNLRNLYRLSKA LFPPEPLVIREMCKQGYRDGLR  
V V FIDA T P Y Y KVK FLHVDI KL LRLCTG L R FV DLK G I LR L AF

FLQRNGLNRPNP-LLALPP-----ARPHGEDKDQAVESAQAE--DYSQLP--GEDH-ILEHLPARINEALLLE  
EEK IC Q G KSSSEGMDPEVAMPSWANMSLDSS SAAL RLEGD LL HLR SILPW ES DT SP AT S

ACVEPTDLLTTLNMLPVRLATAMMVPTPLPESALSFTIRLLEWLDPVPEDIRWMKEQT GSICQ YLVMRAKRLGRHLPS  
EMKDKGGYMSKIC L I IMSYV L C V LAIVQ VT M D VL LQWV SQVFTRVL CLLEPASRSQM V

RLPEQVELRRVQSLPS-VPLSCAAYREALPGWMRNLSLGDALAKWEECQRLLLGLFCTNVAFPPEALMRAPADPAPAPAD  
SSQQA SPTPE DW CWT C PKGCPAETKAEATPRSI RSS NFFLGKVPAGAEGLS --- SFS EKSL-----

PASPOHQLAGPAPLLSTPAPEARPVIGALGL  
-----

E.

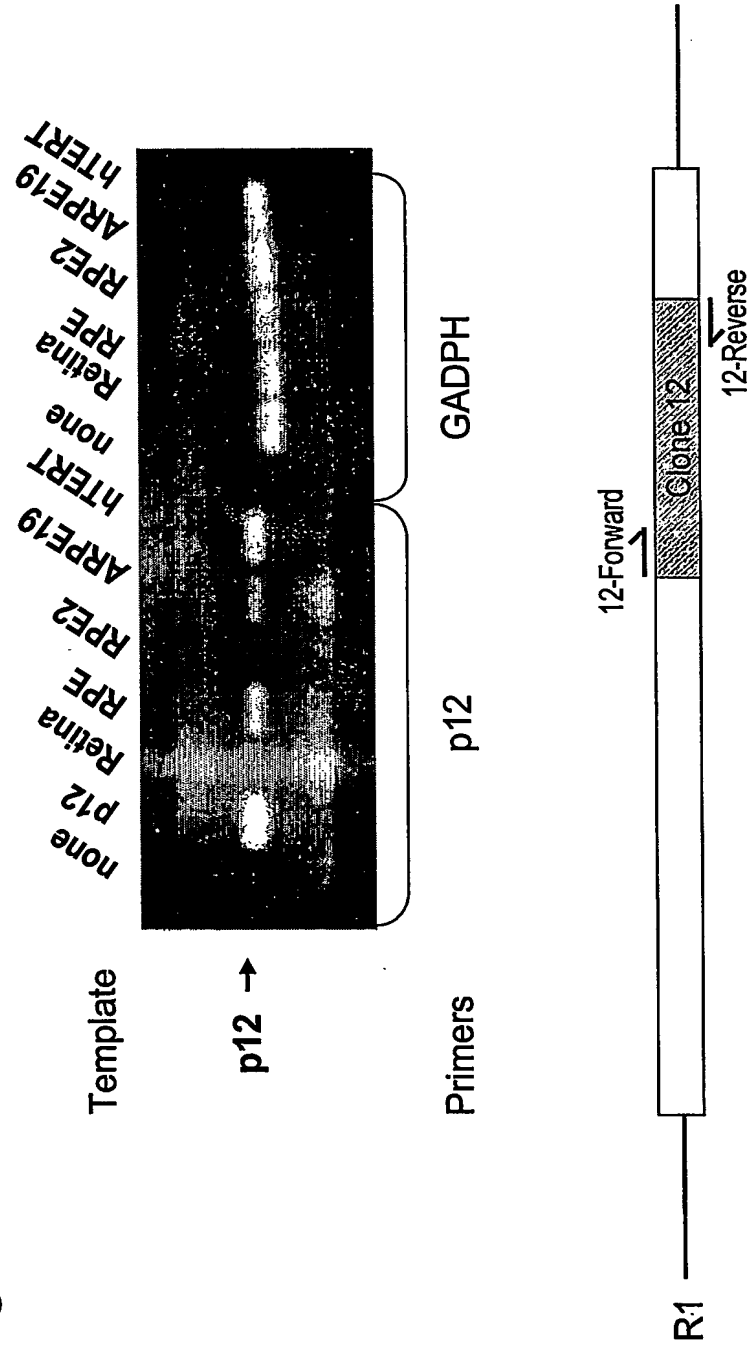
253 GLINRPN PLLALPPARP HGEPKDQAV ESAQAEDYSQ LPGE 293

450 T NVAFPPEALR MRAPADPAPA PADPASPOHQ LAGPAPILST PAPEARPVIG ALGL 504

**Figure 1.**  
**F.**  
**Homologous patatin phospholipase A (PLA) active site in R1: S47 and D166**

Active site serine			
NA	THIYGAS	AGA	LTA R1
YF	DVIGGT	<b>S</b> TGG	LLT Patatin B2
CA	TYVAGL	<b>S</b> GST	WYM cPLA2
Active site aspartic			
SLQ	GVRV	<b>D</b> GGIS	DNLPYE R1
ARY	EFNL	<b>V</b> DGAVA	TVGDPAL Patatin B2
KSK	KIHVV	<b>D</b> SGL-	TFNLPYP cPLA2

Figure 2.



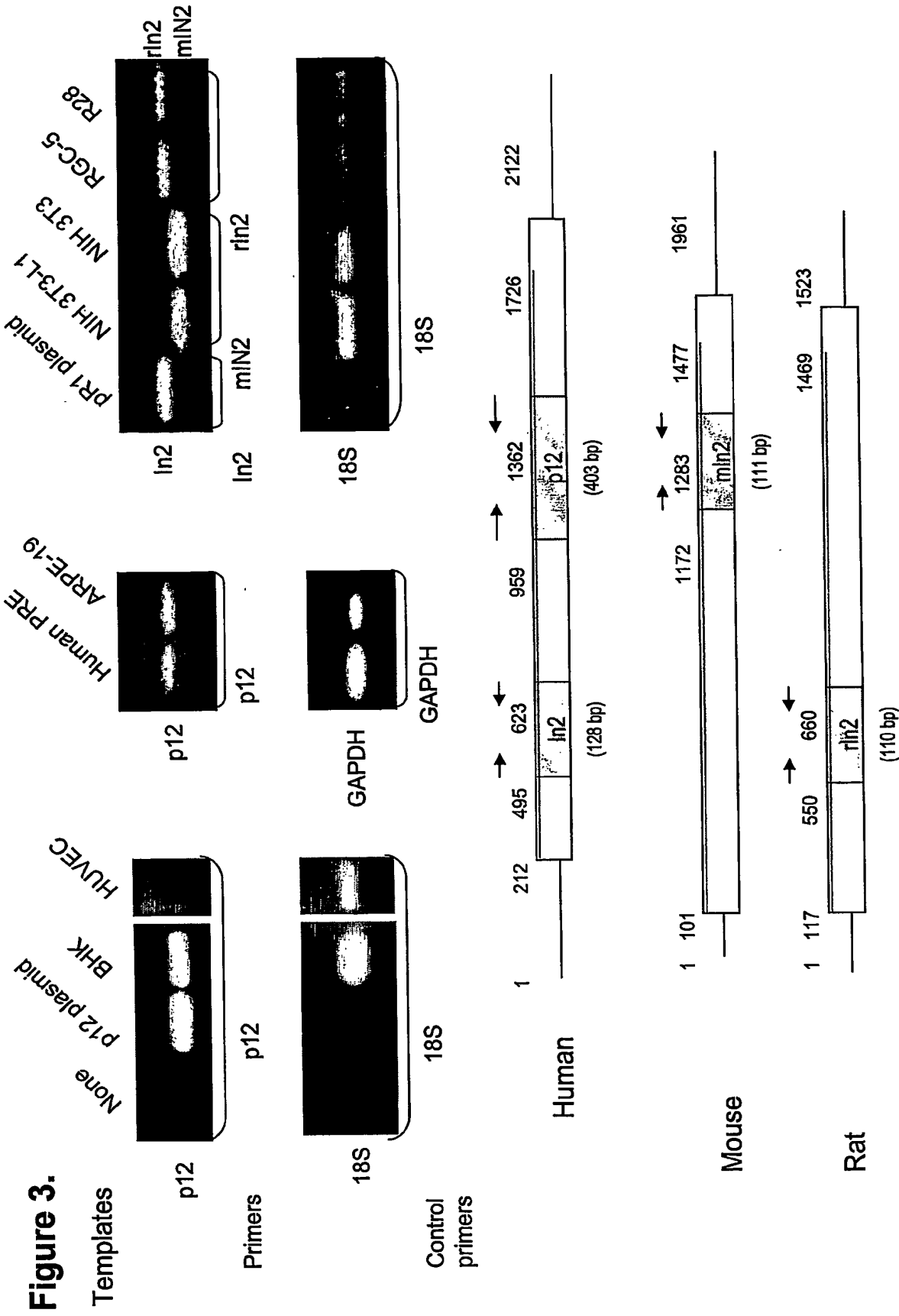
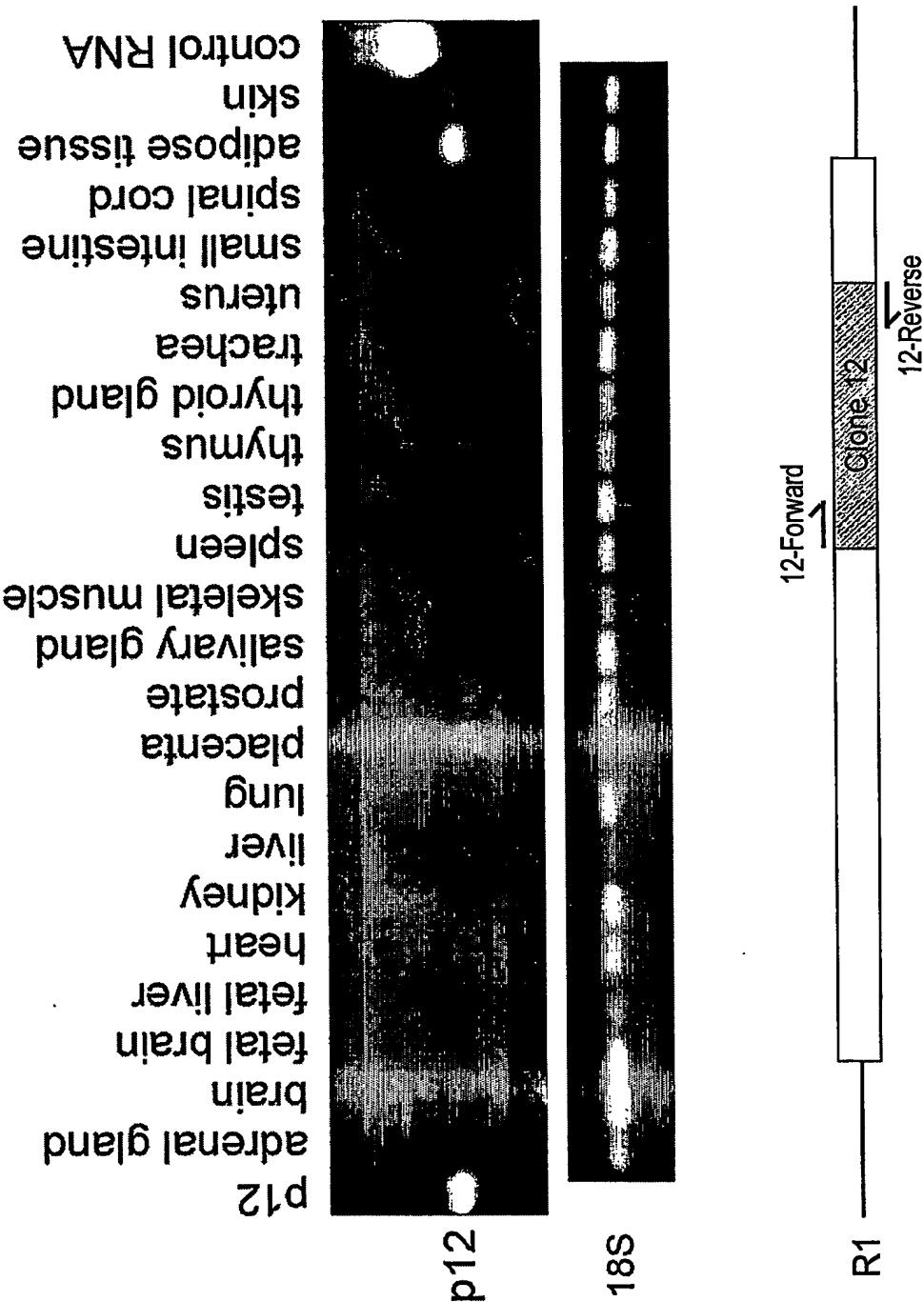


Figure 4.



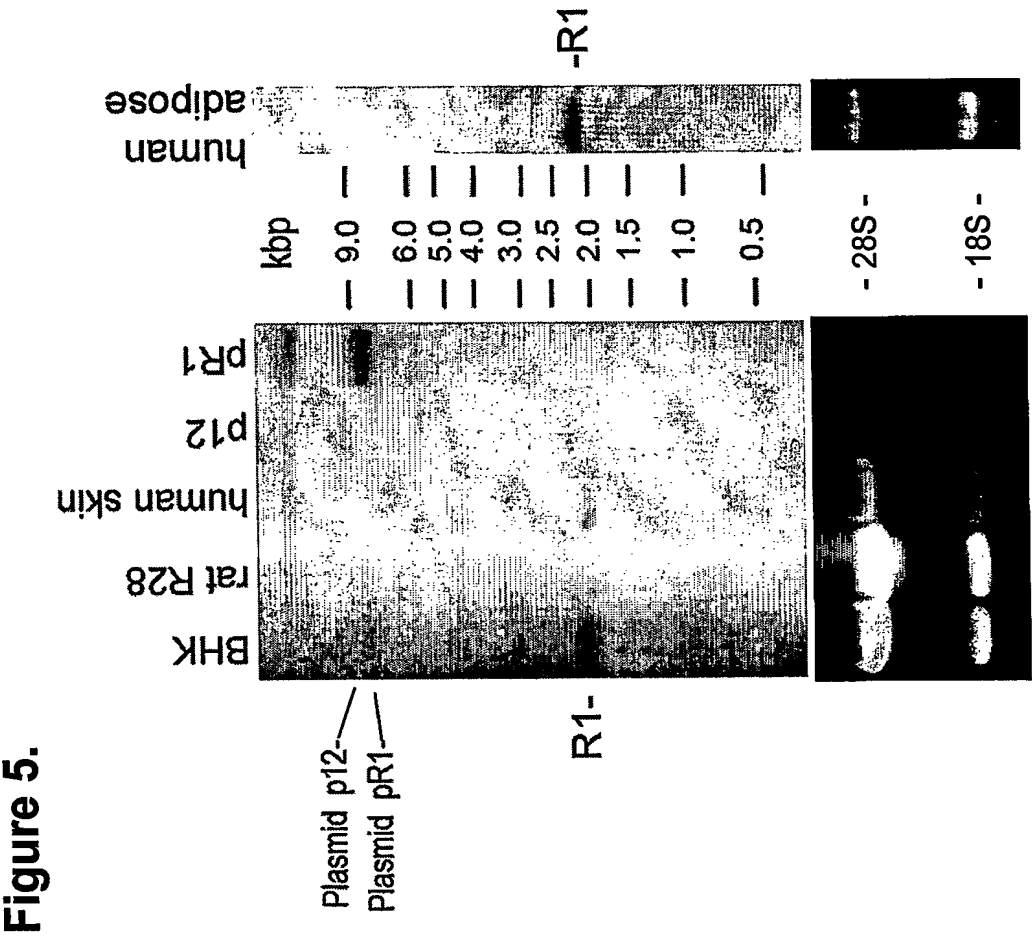
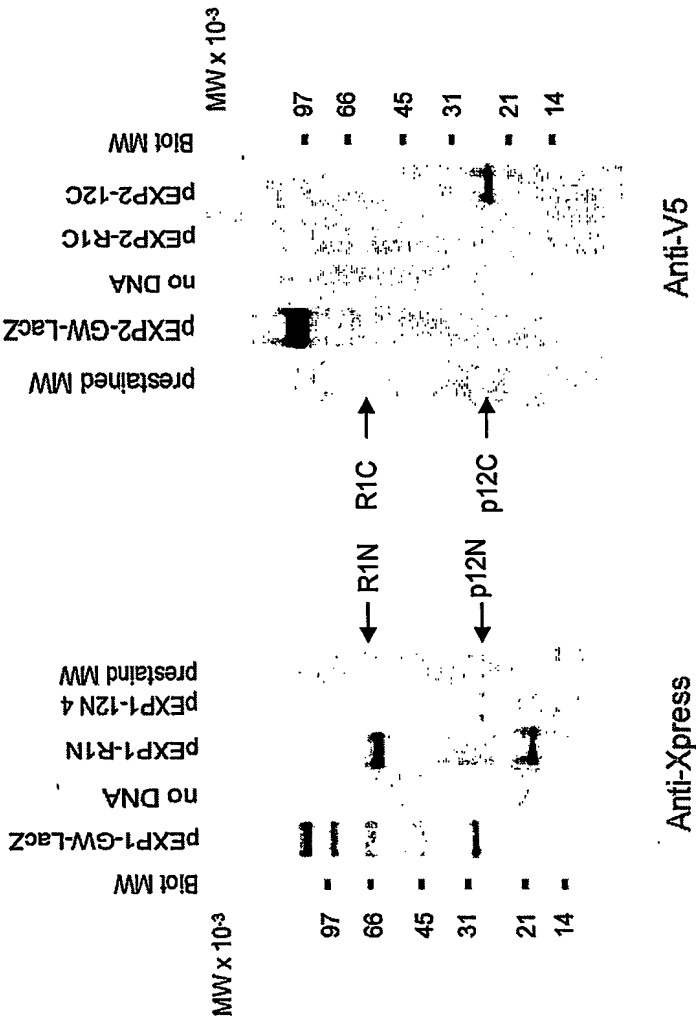






Figure 7.



10/30

Figure 8.

A. p12

Chromatogram

SDS-PAGE  
(Magic Blue stained gel)

Western (Ab-His)

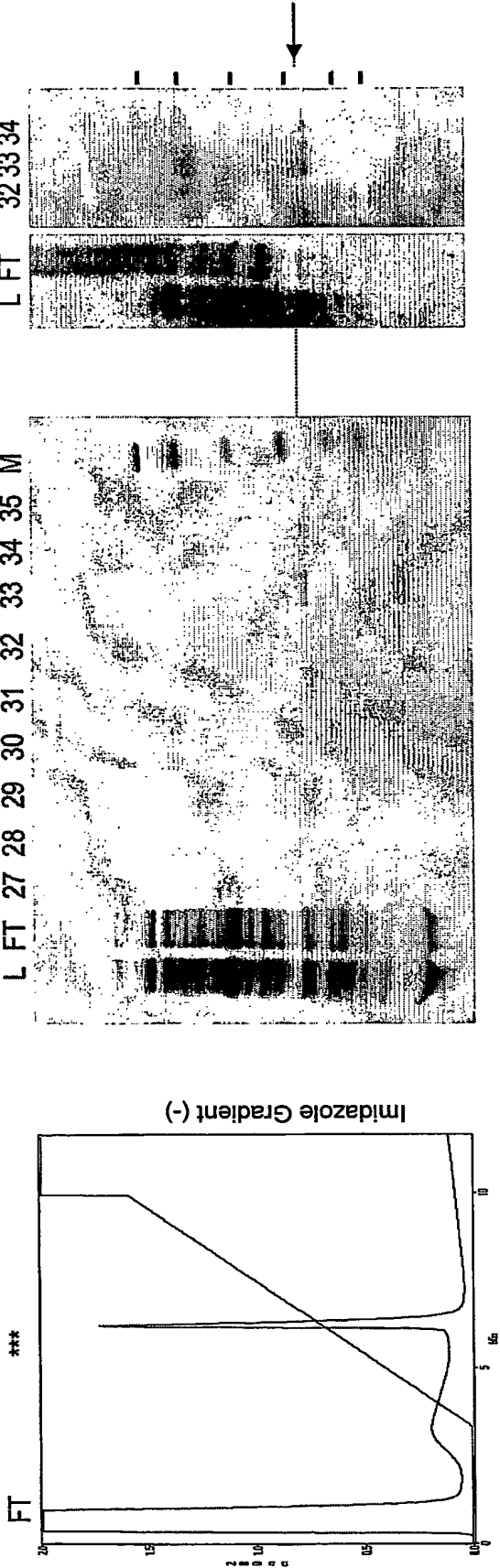
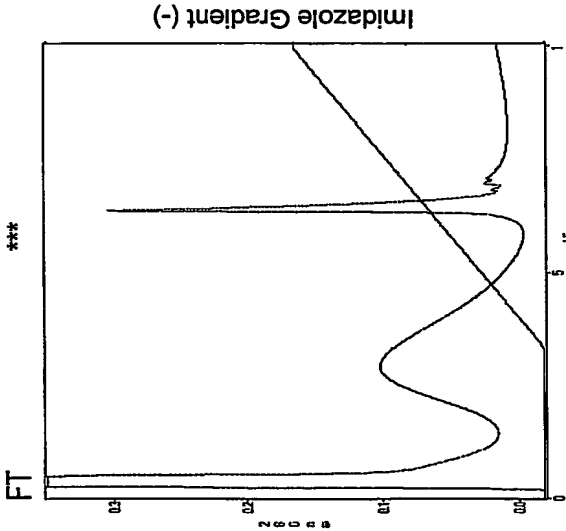


Figure 8.

B. R1

Chromatogram



SDS-PAGE (Coomassie Blue stained gel)

L FT 13 14 15 16 17 18 M

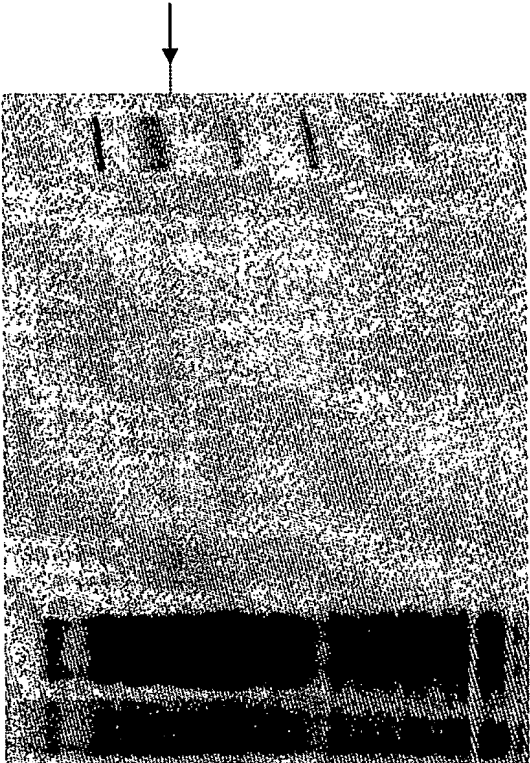


Figure 9.

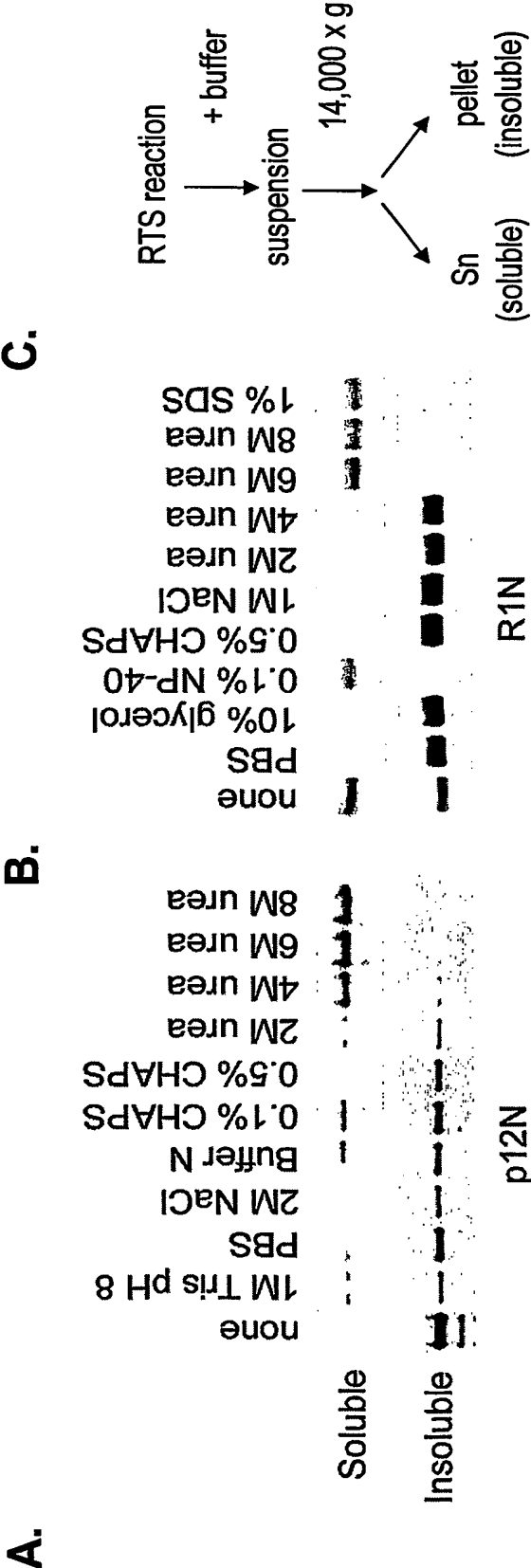
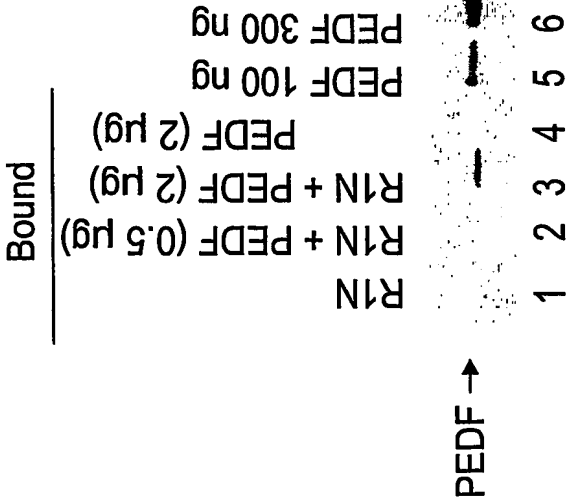


Figure 10.

A. His-tag pull-down



B. complex formation

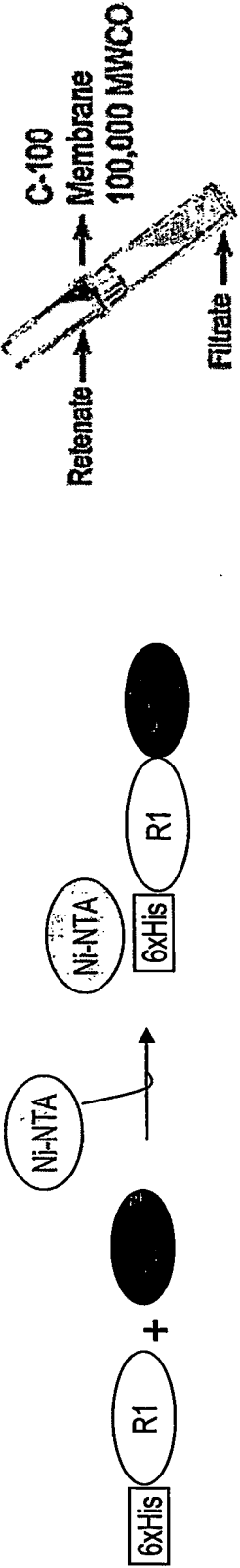
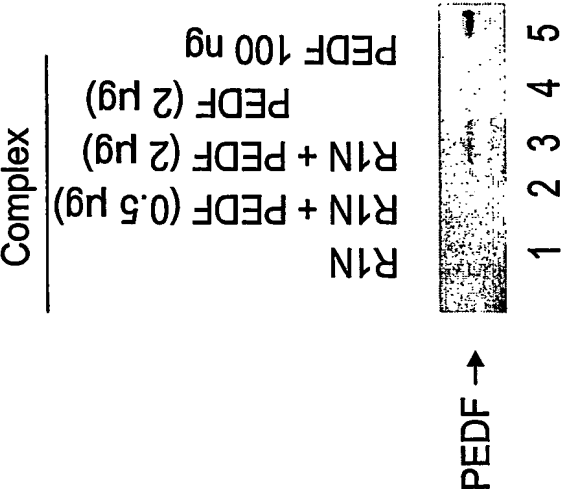
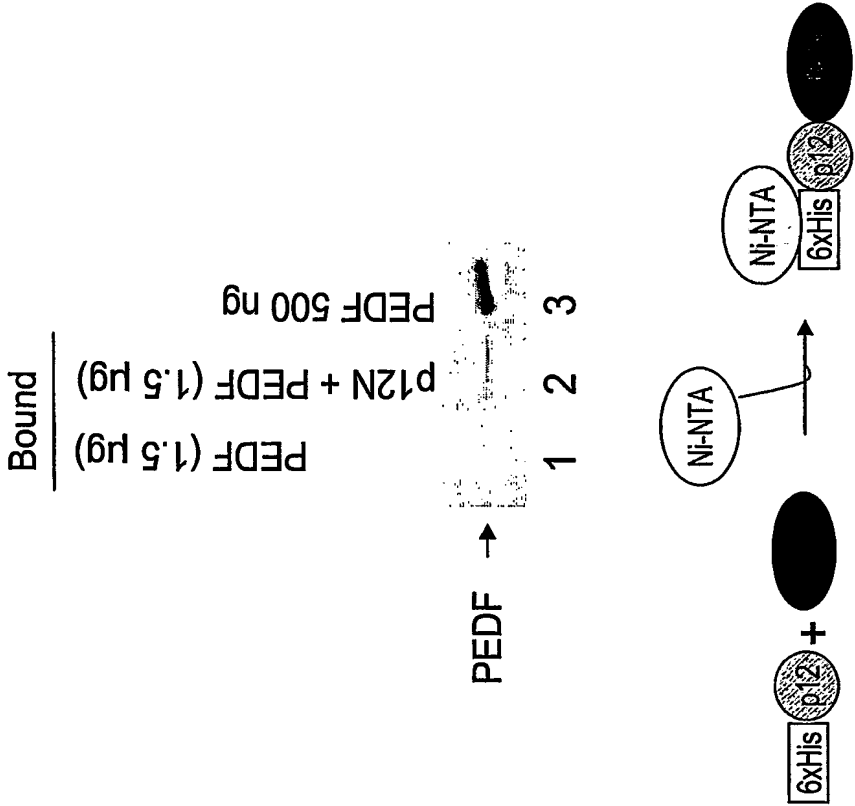


Figure 11.

A.



B.

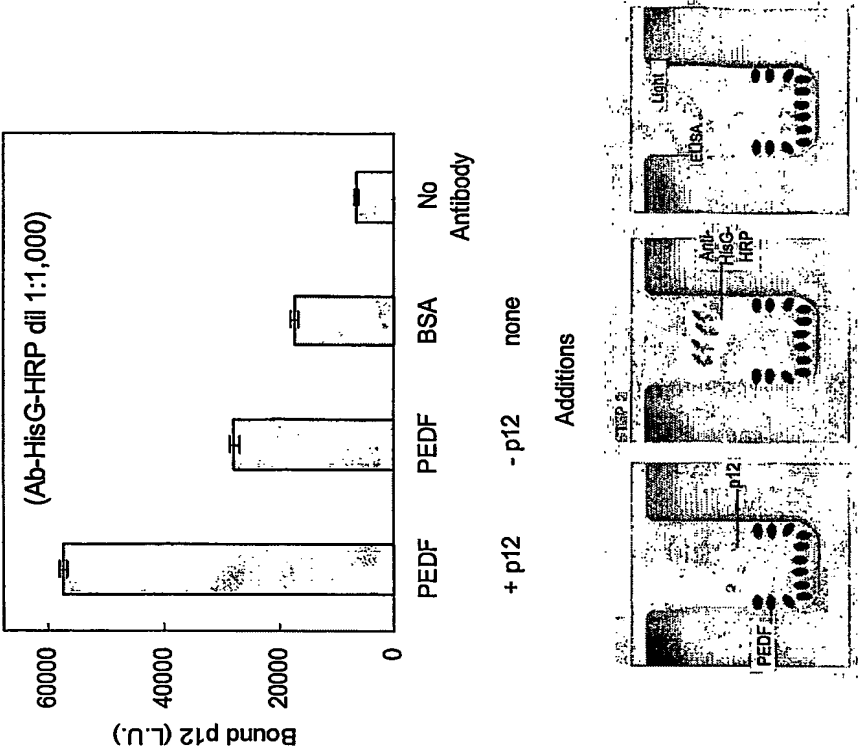


Figure 12.

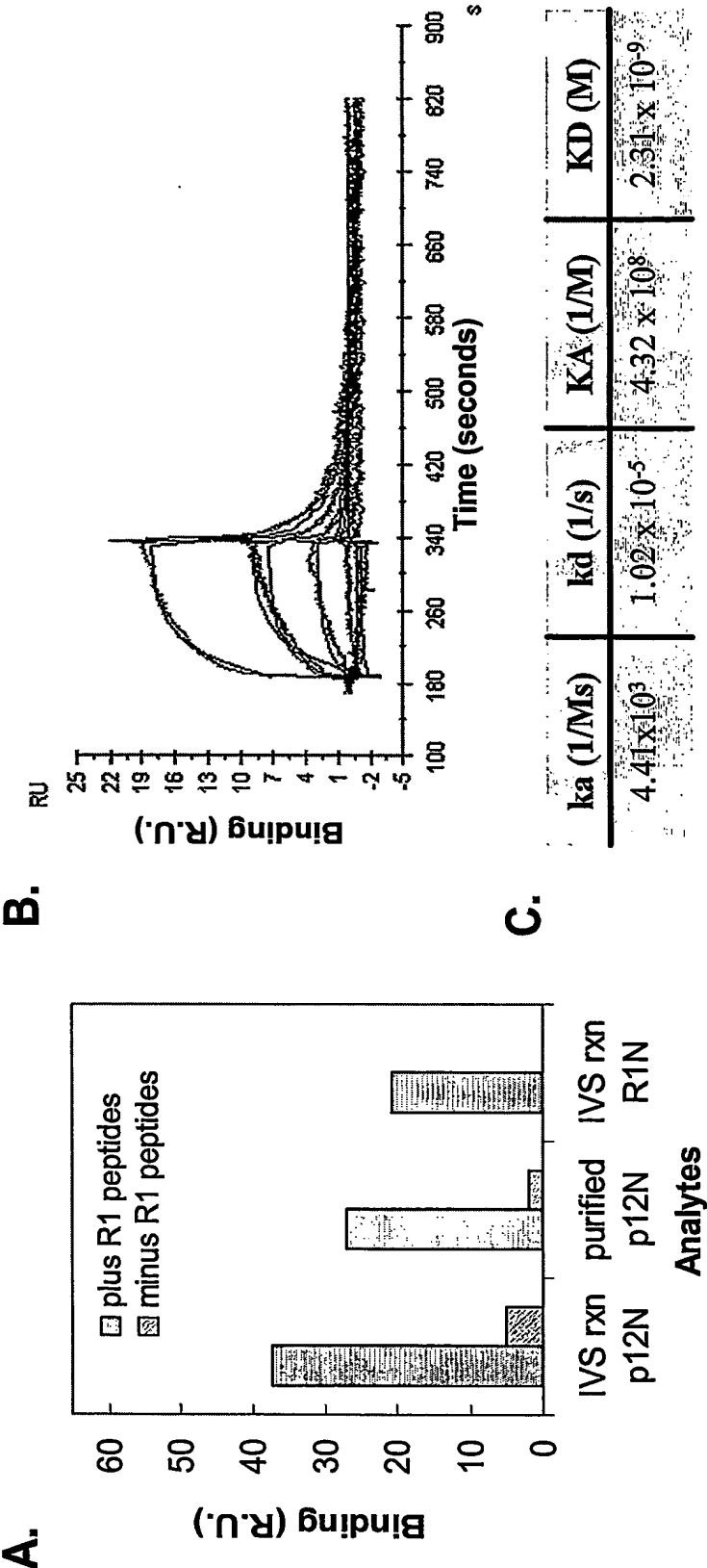


Figure 13.  
A.

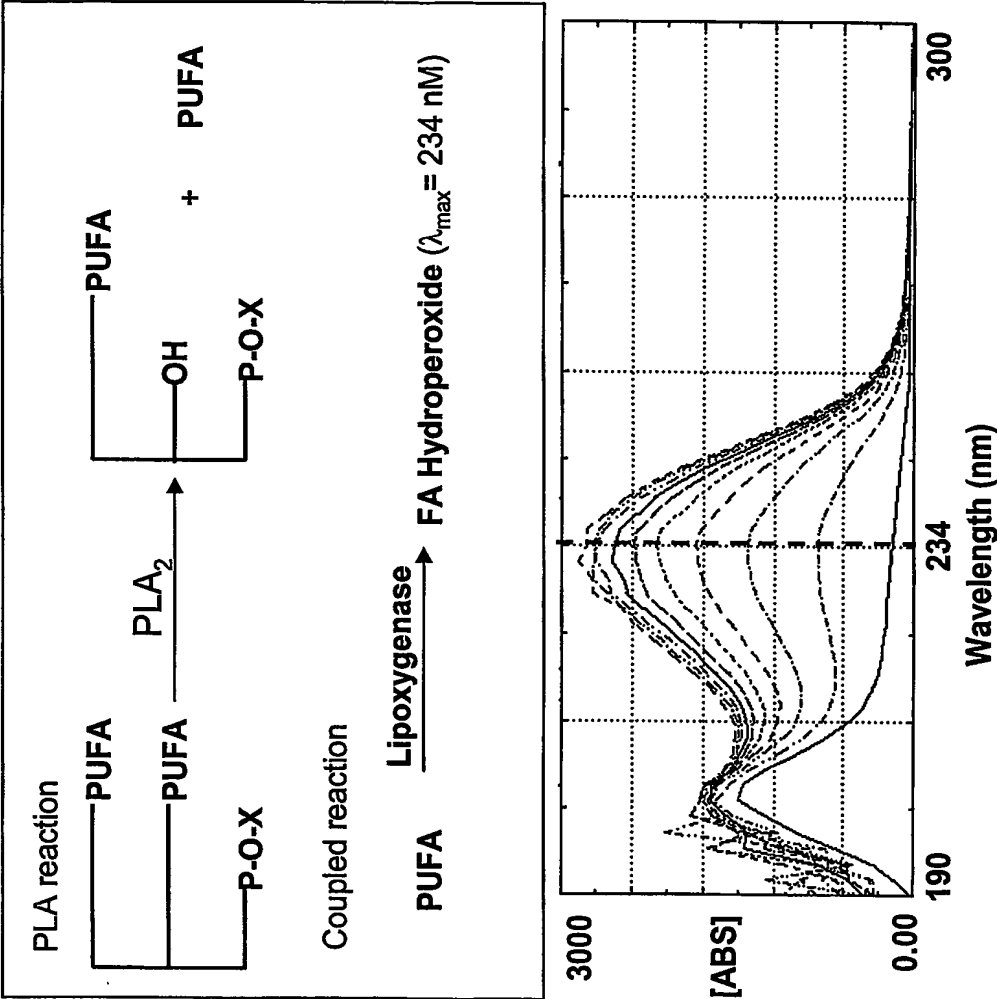
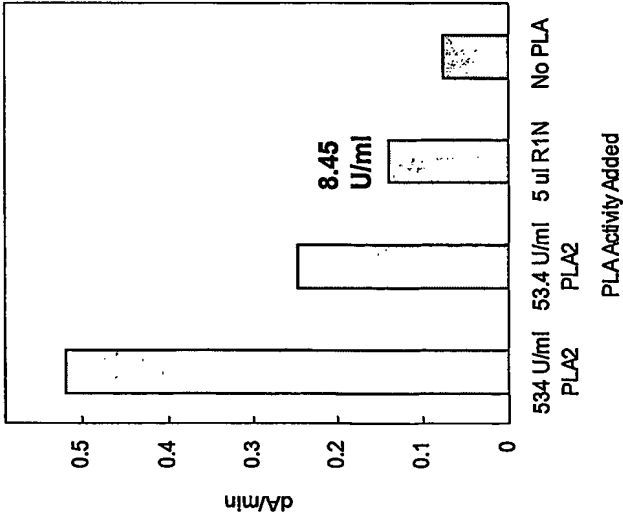


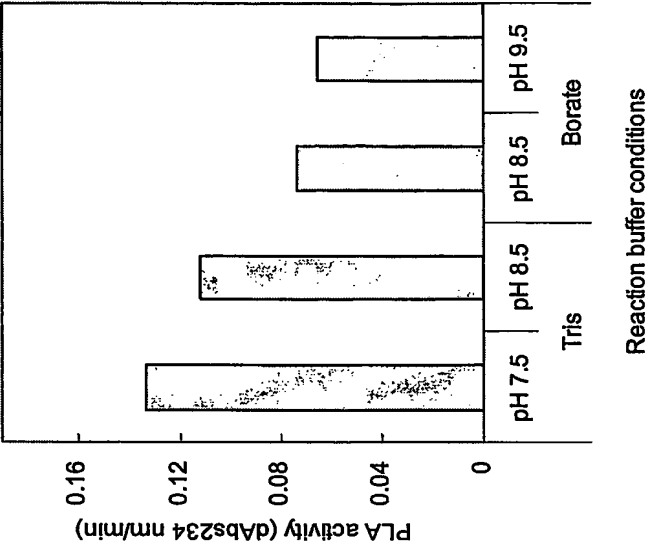


Figure 13.

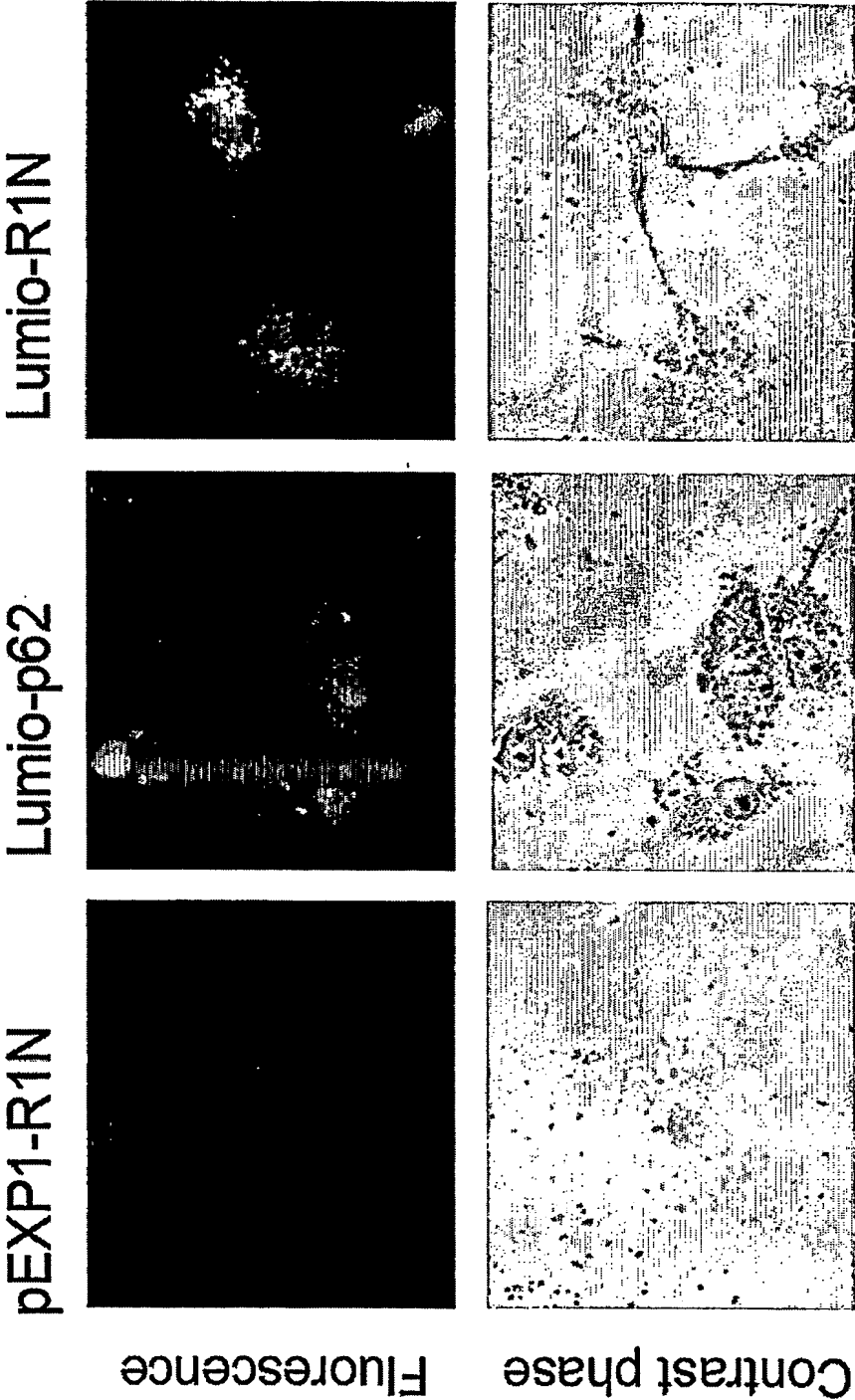
B.



C.



**Figure 14.**  
A. COS-7 cells



**Figure 14.**  
**B. Retinal ganglion RGC-5 cells**

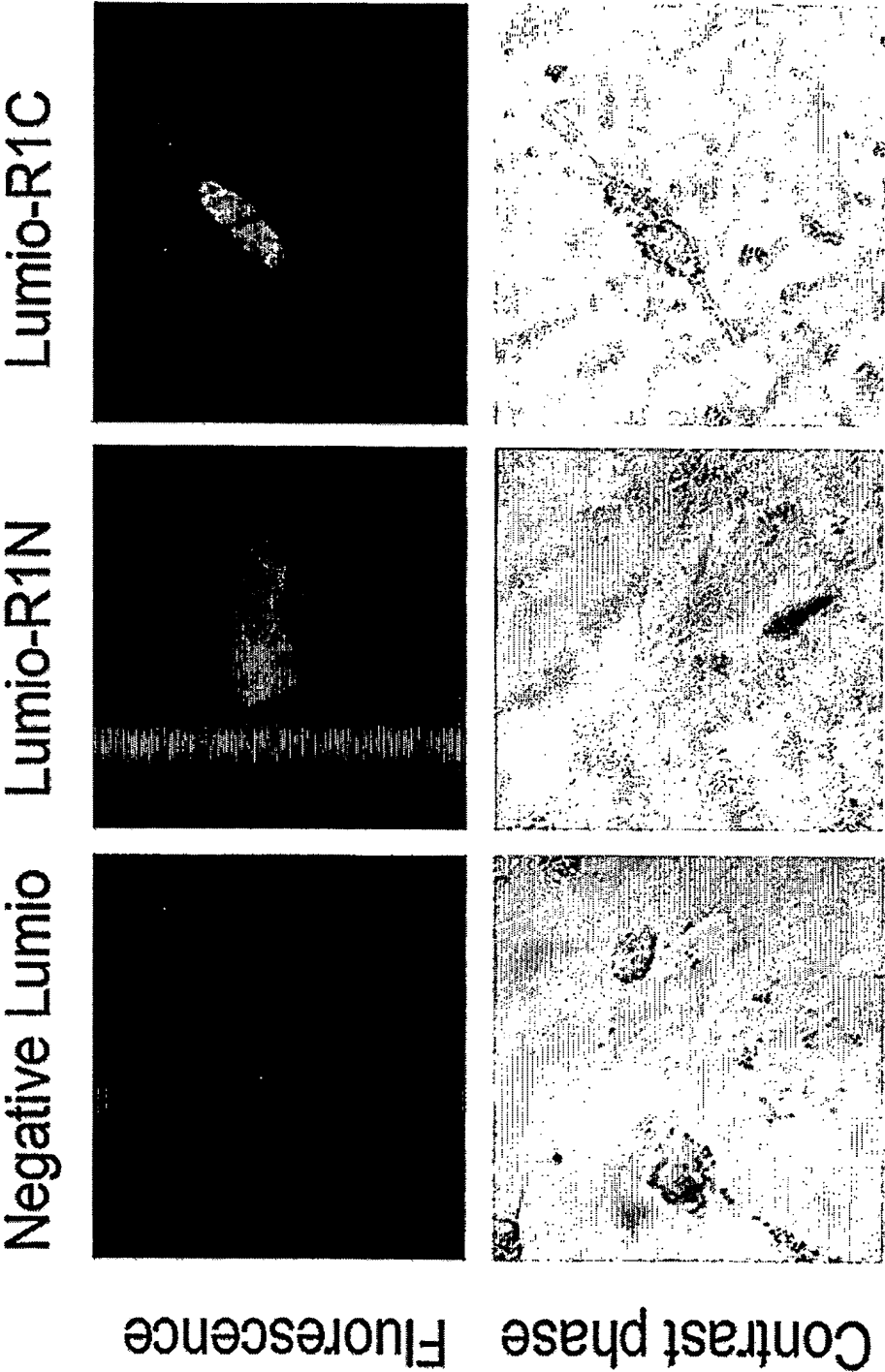


Figure 15.

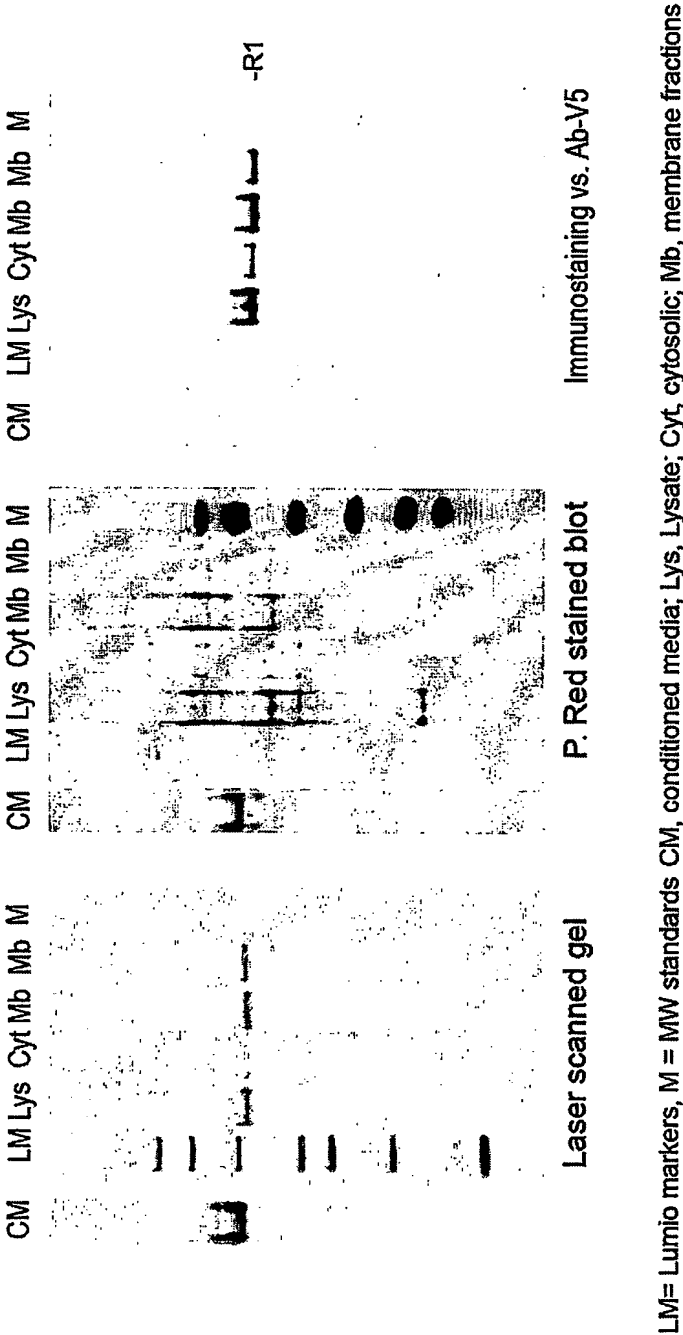


Figure 16.

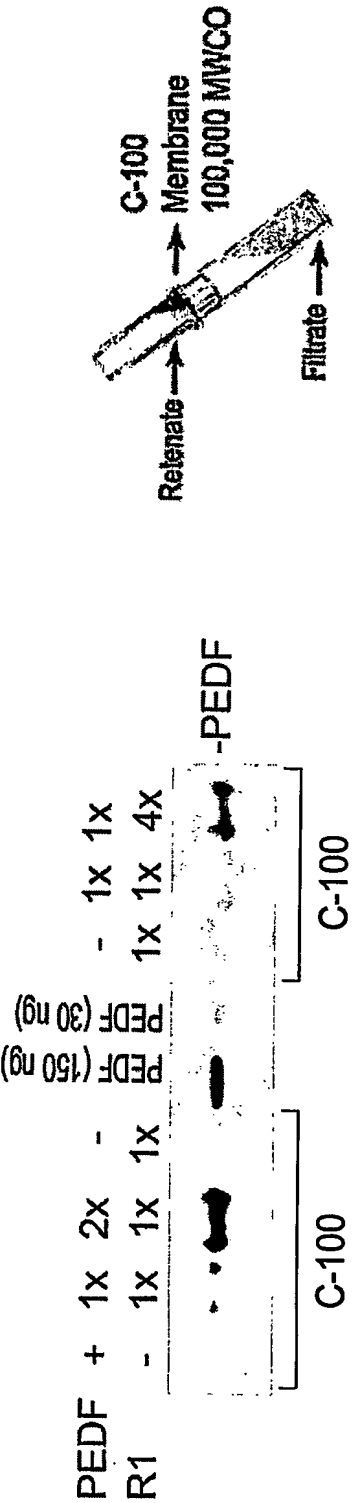


Figure 17.

A.

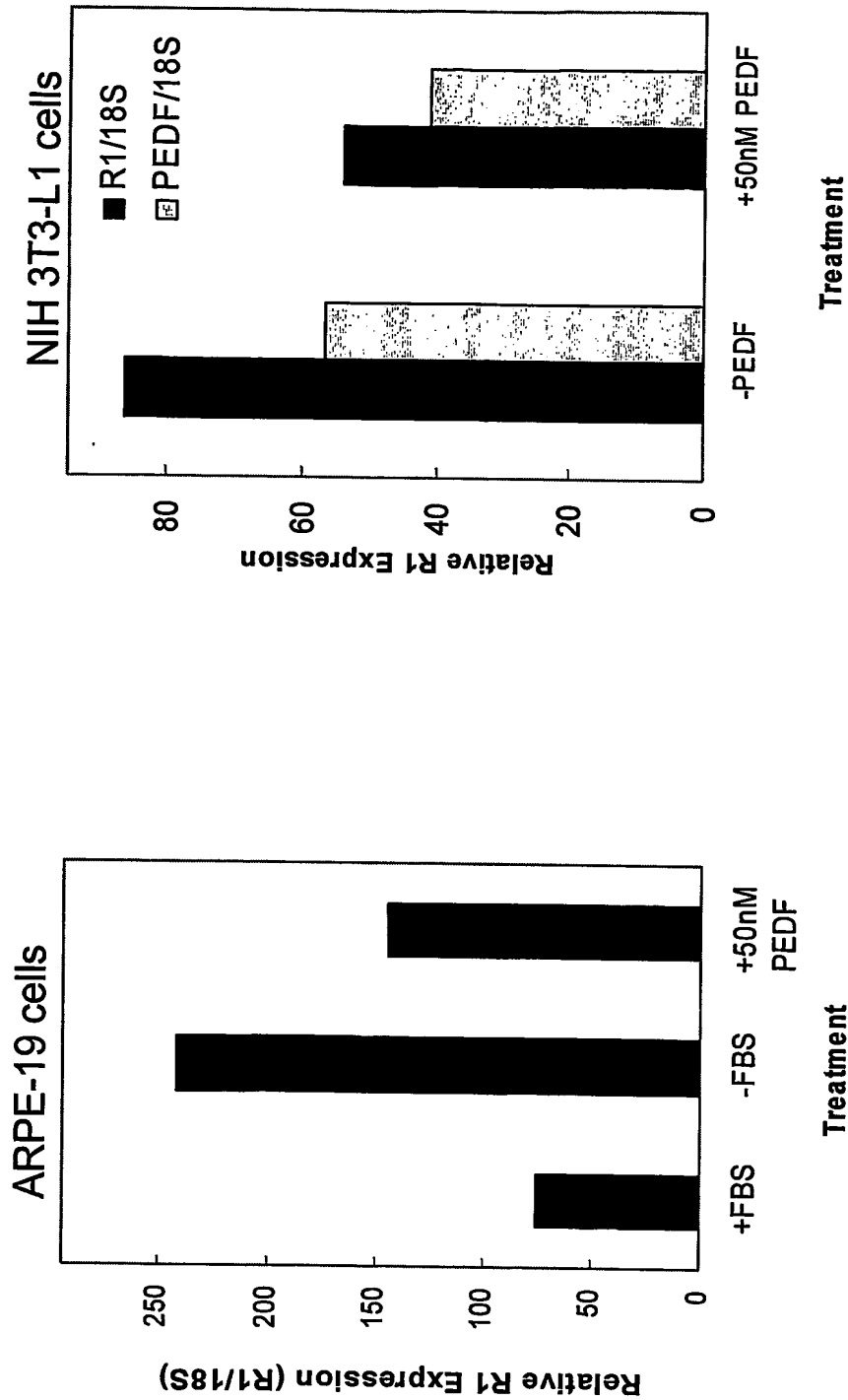


Figure 17.

B.

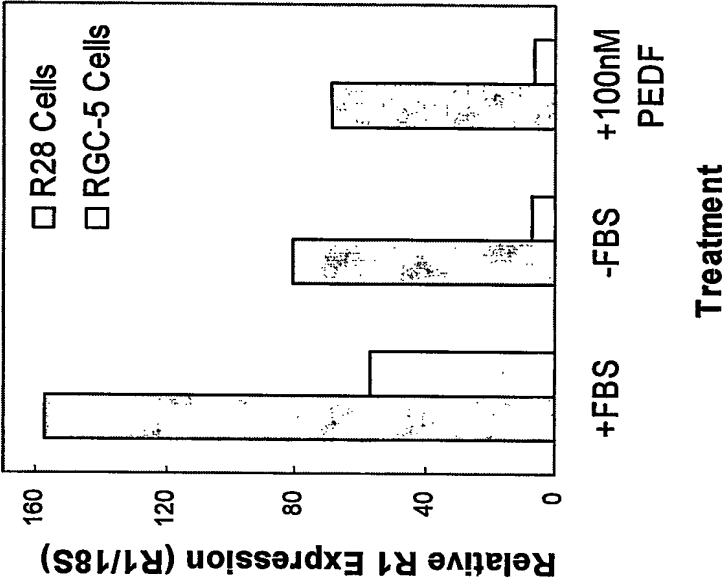


Figure 17.

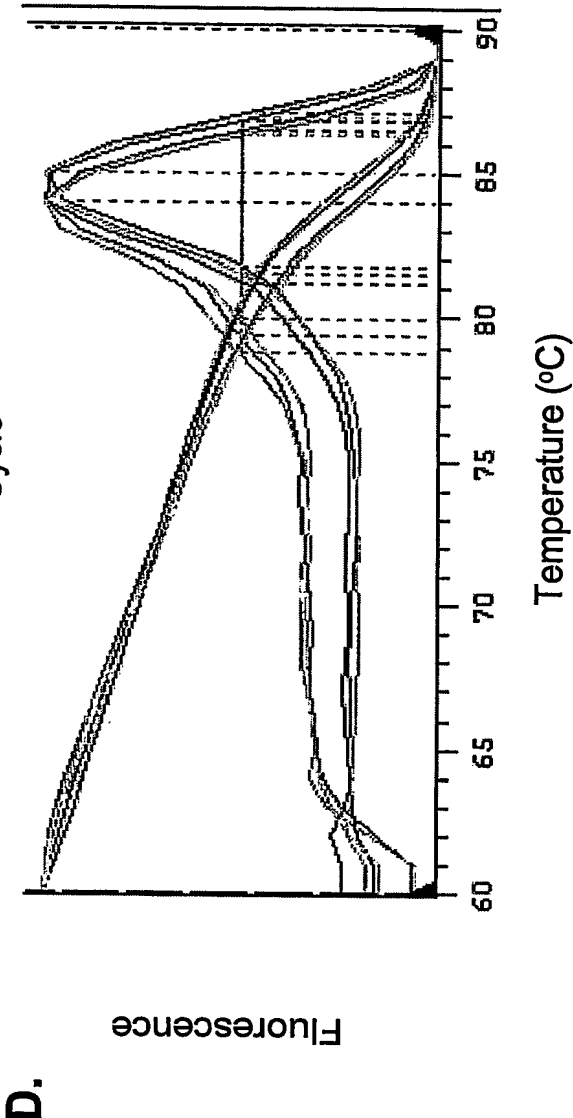
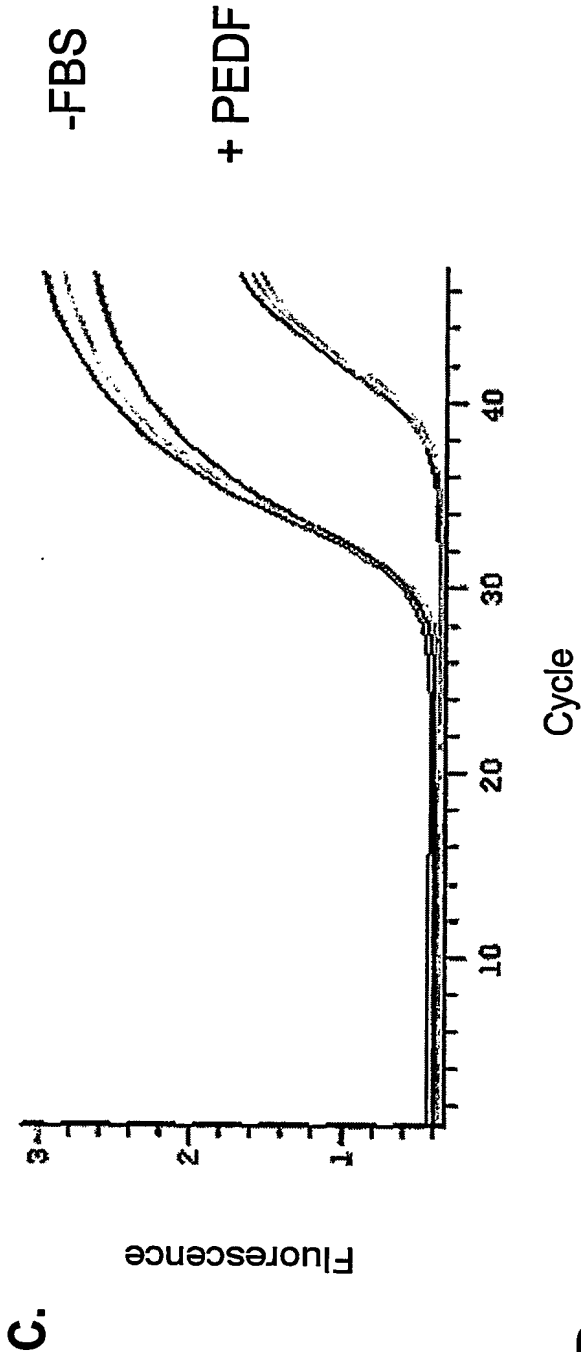
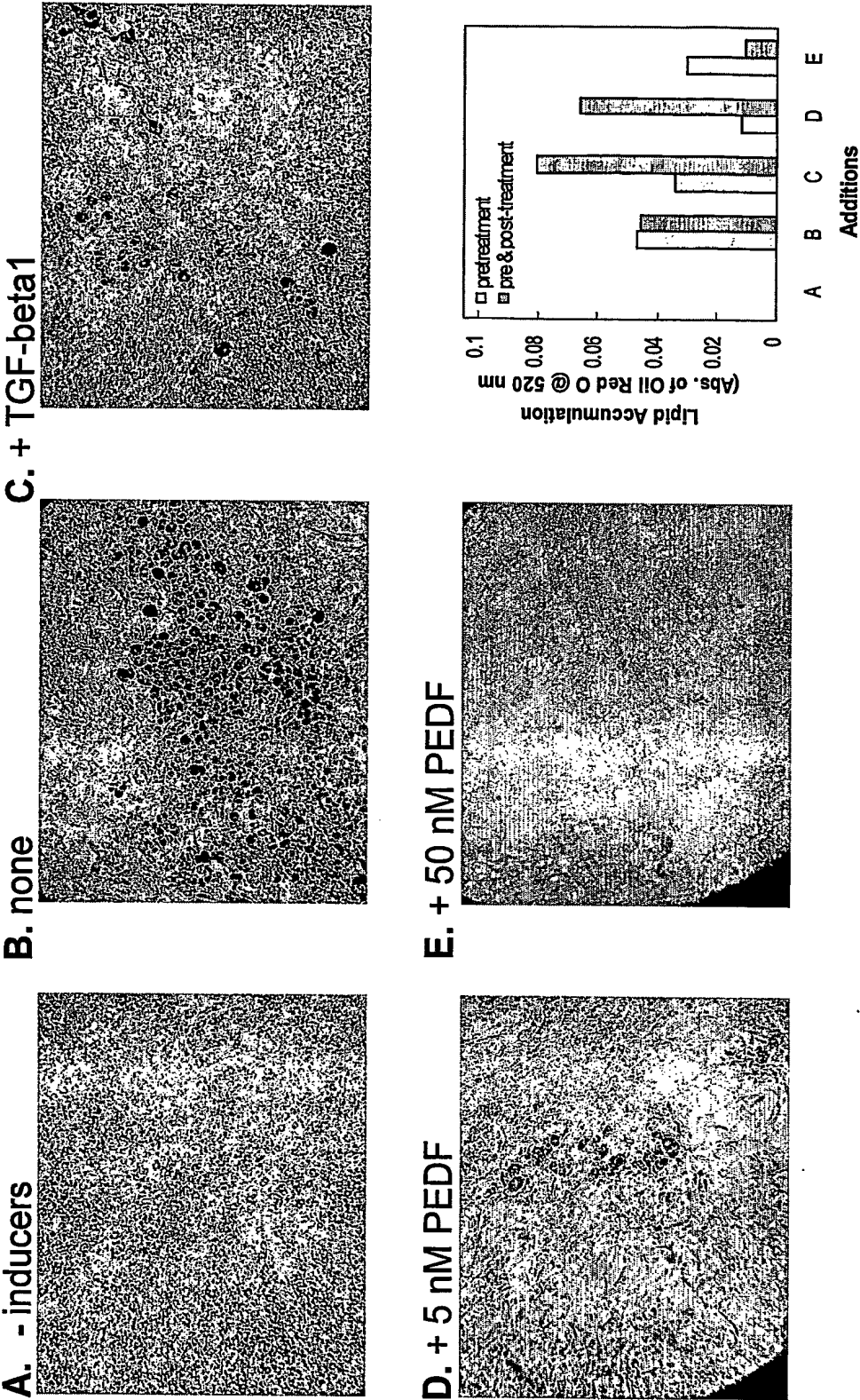




Figure 18.



### Figure 19.

CLUSTAL W (1.82) multiple sequence alignment

gi 26327465 dbj BAC27476.1	MFPRETKWNISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA	50
gi 34861242 ref XP_341961.1	MFPRETKWNISFAGCGFLGVYHIGVASCLREHAPFLVANATHIYGASAGA	50
gi 16878147 gb AAH17280.1	MFPRETKWNISFAGCGFLGVYVGVASCLREHAPFLVANATHIYGASAGA	50
	*****.*****.:*****	
gi 26327465 dbj BAC27476.1	LTATALVTGACLGEAGANIIIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK	100
gi 34861242 ref XP_341961.1	LTATALVTGACLGEAGANIIIEVSKEARKRFLGPLHPSFNLVKTIRGCLLK	100
gi 16878147 gb AAH17280.1	LTATALVTGVCLGEAGAKFIEVSKEARKRFLGPLHPSFNLVKIIRSFLLK	100
	*****.*****.:***** **.	
gi 26327465 dbj BAC27476.1	TLPADCHERANGRLGISLTRVSDGENVIIISHFSSKDELIQANVCSTFIPV	150
gi 34861242 ref XP_341961.1	TLPADCHTRASGRGLISLTRVSDGENVIIISHFSSKDELIQANVCSTFIPV	150
gi 16878147 gb AAH17280.1	VLPADSHHASGRGLISLTRVSDGENVIIISHFNSKDELIQANVCSGFIPV	150
	.****.* :*.*****.***** ****	
gi 26327465 dbj BAC27476.1	YCGLIPPTLQGVRVVDGGISDNPLPLYELKNITITVSPFSGESDIPCQDSST	200
gi 34861242 ref XP_341961.1	YCGLIPPTLQGVRVVDGGISDNPLPLYELKNITITVSPFSGESDIPCQDSST	200
gi 16878147 gb AAH17280.1	YCGLIPPSLQGVRYVDGGISDNPLPLYELKNITITVSPFSGEDIPCQDSST	200
	*****.:*****	
gi 26327465 dbj BAC27476.1	NIHELVRTNTSIQFNLRNLRYLSKALFPPEPMVLREMCKQGYRDGLRFLR	250
gi 34861242 ref XP_341961.1	NIHELRTNTSIQFNLRNLRYLSKALFPPEPMVLREMCKQGYRDGLRFLR	250
gi 16878147 gb AAH17280.1	NIHELVRTNTSIQFNLRNLRYLSKALFPPEPLVREMCKQGYRDGLRFLQ	250
	*****.:*****.:*****:	
gi 26327465 dbj BAC27476.1	RNGLLNQPNPLLALPPVVPQEEDAEEA AVVEERAGEEDQLQPYRKDRILE	300
gi 34861242 ref XP_341961.1	RNGLLNQPNPLLALPPVVPQEEDAEEA AVTEERTGGED-----RILE	292
gi 16878147 gb AAH17280.1	RNGLLNRPNPLLALPPARPHGPEDKDQAVESAQAEDYSQLP--GEDHILE	298
	*****.:*****. *: : :: ** . : :	
gi 26327465 dbj BAC27476.1	HLPARLNEALLEACVEPKDLMTTSLNMLPVRLATAMMVPTYTLPLESAVSF	350
gi 34861242 ref XP_341961.1	HLPARLNEALLEACVEPKDLMTTSLNMLPVRLATAMMVPTYTLPLESAVSF	342
gi 16878147 gb AAH17280.1	HLPARLNEALLEACVEPTDLLTTSLNMLPVRLATAMMVPTYTLPLESALSF	348
	*****.*****.:*****:	
gi 26327465 dbj BAC27476.1	TIRLEWLDPDVPEDIRWMKEQTGSICQYLVMRAKRKLGDHLPSRLSEQVE	400
gi 34861242 ref XP_341961.1	TIRLEWLDPDVPEDIRWMKEQTGSICQYLVMRAKRKLGDHLPSRLSEQVE	392
gi 16878147 gb AAH17280.1	TIRLEWLDPDVPEDIRWMKEQTGSICQYLVMRAKRKLGRHLPSRLPEQVE	398
	*****.*****	
gi 26327465 dbj BAC27476.1	LRRAQSLPSVPLSCATYSEALPNWVRNNLSLGDALAKWEECQRQLLLGLF	450
gi 34861242 ref XP_341961.1	LRRAQSLPSVPLSCATYSEALPNWVRNNLSLGDALAKWEECQRQLLLGLF	442
gi 16878147 gb AAH17280.1	LRRVQSLPSVPLSCAAYREALPGWMRNNSLGDALAKWEECQRQLLLGLF	448
	***.*****.:* ***. *:*****	
gi 26327465 dbj BAC27476.1	CTNVAFPPDALRM RAPAS--PTAADPATPDPPGLPPC-----	486
gi 34861242 ref XP_341961.1	CTNVAFPPDALRM RAPAS--PTATDPATPDPSGLPPC-----	478
gi 16878147 gb AAH17280.1	CTNVAFPPEALRM RAPADPAPAPADPAS PQHLAGPAPLLSTPAPEARPV	498
	*****.:*****. *.:****:*.	
gi 26327465 dbj BAC27476.1	-----	
gi 34861242 ref XP_341961.1	-----	
gi 16878147 gb AAH17280.1	IGALGL 504	

## Figure 20. (1 of 4)

CLUSTAL W (1.82) multiple sequence alignment

```
gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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GGCACGAGGGCGGCCCCAGTCAGACGCAGGCAGCCCCAAAGCCTGAACAG 50

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
GCAGGGCCAGACCCAGCTTCTTCGCCTCCGCCAGCGGGGACCCCGAGCTA 100

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
-----TCCTCTGCCTCCCGGCACAGCGTCTCCGCCTCCG 34
GAGCCGCAGCGGGACCTGCCCGGCCCCCGGCTCCAGCGAGCGAGCGGCGA 150

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
-----GGAGACCCCAAGGTATCGA-GACTGCGGGACCCACTGCCCGCAGG 44
CCGGCGGGGACCCAGGTTATCAA-GACTGCGGGACCCACTGCCCGCAGG 83
GCAGCGCGCTCACAGAGCCTGGCCGCCACGGAACCCGGGGCCCGGCGG 200
* * * * * * * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
ACATCGAGTCACGATGTTCCCGAGGGAGACCAAGTGGAACATCTCATTCG 94
ACGTCTAATCACGATGTTCCCAAGGGAGACCAAGTGGAACATCTCGTTTCG 133
CCGCC--GCCGCGATGTTTCCCGCGGAGAACGCTGGAACATCTCGTTTCG 248
* * * * * * * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
CTGGCTGCGGCTTCTCTCGGGGTCTACCACATTGGCGTGGCCTCTGCCTC 144
CTGGCTGCGGCTTCTCTCGGGGTCTACCACATTGGAGTGGCCTCTGCCTC 183
CGGGCTGCGGCTTCTCTCGGGGTCTACTACGTCGGCGTGGCCTCTGCCTC 298
* * * * * * * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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CGTGAGCACGCGCCCTTCTGGTGGCCAAACGCCACTCACATCTACGGAGC 194
CGTGAGCACGCGCCCTTCTGGTGGCCAAACGCCACTCACATCTACGGAGC 233
CGCGAGCACGCGCCCTTCTGGTGGCCAAACGCCACGCACATCTACGGCGC 348
** * * * * * * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
CTCGGCAGGGGCGCTCACCGCCACAGCGCTGGTCACTGGGGCCTGCCTGG 244
CTCGGCAGGGGCGCTTACCGCCACAGCGCTGGTCACTGGGGCCTGCCTGG 283
CTCGGCCGGGGCGCTCACCGCCACGGCGCTGGTCACCGGGGTCTGCCTGG 398
***** * * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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GCGAAGCGGGTGCCAACATTATTGAGGTGTCCAAGGAGGCTCGGAAGCGG 333
GTGAGGCTGGTGCCAAAGTTCATTGAGGTATCTAAAGAGGCCCGGAAGCGG 448
* * * * * * * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
-----
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TTCCTGGGCCCCCTGCACCCCTCCTTCAACCTGGTAAAGATCATCCGCAG 498
***** * * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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CTGTCTACTAAAGACCCTGCCTGCTGATGTCATGAGCGCGCCAAATGGAC 394
TTGTCTACTGAAGACCCTGCCTGCTGATGTCATGAGCGCGCCAAATGGAC 433
TTTCTGTCTGAAGTCTCTGCCTGCTGATGTCATGAGCATGCCAGTGGGC 548
* * * * * * * * * * * * * * * * * * * * * * * * * * * *

gi|26327464|dbj|AK031609.1|
gi|34861241|ref|XM_341960.1|
gi|16878146|gb|BC017280.1|BC01
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GCCTGGGCATCTCCCTGACTCGTGTTCAGACGGAGAGAACGTCATCATA 444
GCCTGGGCATCTCCCTGACTCGAGTTTCGGATGGAGAGAAATGTCATCATA 483
GCCTGGGCATCTCCCTGACCCGCGGTGTACAGCGCGAGAAATGTCATTATA 598
***** * * * * * * * * * * * * * * * * * * * * * * *
```

**Figure 20. (2 of 4)**

gi 26327464 dbj AK031609.1	TCCCACTTTAGCTCCAAGGATGAGCTCATCCAGGCCAATGCTGTCAGCAC	494
gi 34861241 ref XM_341960.1	TCGCACCTTTAGCTCCAAGGATGAGCTTATCCAGGCCAATGTTGTCAGCAC	533
gi 16878146 gb BC017280.1 BC01	TCCCACTTCAACTCCAAGGACGAGCTCATCCAGGCCAATGCTGTCAGCGG	648
	** ***** *	
gi 26327464 dbj AK031609.1	ATTTATCCCGGTGTACTGTGGCCTCATTCTCTACCTCCAAGGGGTGC	544
gi 34861241 ref XM_341960.1	TTTTATCCCTGTGTACTGTGGCCTCATTCTCTACCTTCAAGGGGTGC	583
gi 16878146 gb BC017280.1 BC01	TTTCATCCCCGTGTACTGTGGGCTCATCTCTCCCTCCCTCCAGGGGTGC	698
	** ***** *	
gi 26327464 dbj AK031609.1	GCTATGTGGATGGCGGCATTTTCAGACAACCTTGCCACTTTATGAGCTGAAG	594
gi 34861241 ref XM_341960.1	GCTATGTGGATGGCGGCATTTTCAGACAACCTTGCCACTTTATGAGCTGAAG	633
gi 16878146 gb BC017280.1 BC01	GCTACGTGGATGGTGGCATTTTCAGACAACCTTGCCACTCTATGAGCTTAAG	748
	**** ***** *	
gi 26327464 dbj AK031609.1	AATACCATCACAGTGTCCCCATTCTCAGGCGAGAGTGACATCTGCCCTCA	644
gi 34861241 ref XM_341960.1	AATACCATCACAGTGTCCCCATTCTCAGGCGAGAGTGACATCTGCCCTCA	683
gi 16878146 gb BC017280.1 BC01	AACACCATCACAGTGTCCCCCTTCTCGGGCGAGAGTGACATCTGTCCGCA	798
	** ***** *	
gi 26327464 dbj AK031609.1	GGACAGCTCCACCAACATCCACGAGCTTCGCGTCACCAACACCAGCATCC	694
gi 34861241 ref XM_341960.1	AGACAGCTCCACCAACATCCACGAACCTTCGTATCACCAACACCAGCATCC	733
gi 16878146 gb BC017280.1 BC01	GGACAGCTCCACCAACATCCACGAGCTGCGGGTCACCAACACCAGCATCC	848
	***** ** *	
gi 26327464 dbj AK031609.1	AGTTCAACCTTCGCAATCTCTACCGCCTCTCGAAGGCTCTCTCCCGCCA	744
gi 34861241 ref XM_341960.1	AATTCAACCTTCGCAATCTCTACCGCCTCTCGAAGGCTCTCTCCCGCCA	783
gi 16878146 gb BC017280.1 BC01	AGTTCAACCTTCGCAACCTCTACCGCCTCTCGAAGGCTCTCTCCCGCCG	898
	* ***** *	
gi 26327464 dbj AK031609.1	GAGCCCATGGTCTCCGAGAGATGTGCAACAGGGCTACAGAGATGGACT	794
gi 34861241 ref XM_341960.1	GAGCCCATGGTCTCTCCGAGAGATGTGCAACAGGGCTACCGAGATGGACT	833
gi 16878146 gb BC017280.1 BC01	GAGCCCTGGTGTCTGCGAGAGATGTGCAAGCAGGGATACCGGGATGGCCT	948
	***** ** *	
gi 26327464 dbj AK031609.1	TCGATTCTTAGGAGGAATGGCCTACTGAACCAACCCAACCCCTTTGCTGG	844
gi 34861241 ref XM_341960.1	TCGATTCTTAGGAGGAATGGCCTACTGAACCAACCCAACCCCTTTGCTGG	883
gi 16878146 gb BC017280.1 BC01	GCGCTTTCTGCAGCGGAACGGCCTCCTGAACCGGCCAACCCCTTTGCTGG	998
	** ** *	
gi 26327464 dbj AK031609.1	CAC TGCCCCCAGTTGTCCCCCAGGAAGAGGATGCAGAGGAAGCTGCTGTG	894
gi 34861241 ref XM_341960.1	CAC TGCCCCCGTTGTCCCCCAGGAAGAGGATGCAGAGGAAGCTGCCGTG	933
gi 16878146 gb BC017280.1 BC01	CGTTGCCCCCGCCCCCCCCACGG-----CCAGAGGACAAGGACCAG	1042
	* ***** *	
gi 26327464 dbj AK031609.1	GTGGAGGAGAGGGCTGGAGAGGAGGATCAATTGCGACCTTATAGAAAAGA	944
gi 34861241 ref XM_341960.1	ACTGAGGAGAGGACTGGAGGGGAGGATC-----	961
gi 16878146 gb BC017280.1 BC01	GCA GTGGAGAGCGCCCAAGCGGAGGATTACTCGCAGCTGCCGGGAGAAGA	1092
	* ***** *	
gi 26327464 dbj AK031609.1	TCGAATTCTAGAGCACCTGCCCTGCCAGACTCAATGAGGCCCTGCTGGAGG	994
gi 34861241 ref XM_341960.1	--GGATTCTAGAGCACCTGCCCTGCCAGACTCAACGAGGCCCTGCTGGAGG	1009
gi 16878146 gb BC017280.1 BC01	TCACATCTTGAGCACCTGCCCGCCCGCTCAATGAGGCCCTGCTGGAGG	1142
	** ** *	
gi 26327464 dbj AK031609.1	CCTGTGTGGAACCAAGGACCTGATGACCACCCCTTTCCAACATGCTACCA	1044
gi 34861241 ref XM_341960.1	CCTGTGTGGAACCGAAGACCTGATGACCACCCCTTTCCAACATGCTGCCA	1059
gi 16878146 gb BC017280.1 BC01	CCTGCGTGGAGCCACGACCTGCTGACCACCTCTCCAACATGCTGCCT	1192
	**** ***** *	

**Figure 20. (3 of 4)**

```
gi|26327464|dbj|AK031609.1|      GTGCGCCTGGCAACGGCCATGATGGTGCCCTATACTCTGCCGCTGGAGAG 1094
gi|34861241|ref|XM_341960.1|      GTGCGCCTGGCCACTGCCATGATGGTACCTATACTCTGCCACTGGAGAG 1109
gi|16878146|gb|BC017280.1|BC01    GTGCGCTTGCCACGGCCATGATGGTGCCCTACACGCTGCCGCTGGAGAG 1242
***** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      TGCAGTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCTGATGTCCCTG 1144
gi|34861241|ref|XM_341960.1|      CGCAGTGTCTTCACCATCCGTTTGTGGAGTGGCTGCCTGATGTCCCTG 1159
gi|16878146|gb|BC017280.1|BC01    CGCTCTGTCTTCACCATCCGCTTGTGGAGTGGCTGCCCGACGTTCCTG 1292
** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      AAGATATCCGGTGGATGAAAGAGCAGACGGGTAGCATCTGCCAGTATCTG 1194
gi|34861241|ref|XM_341960.1|      AGGATATCCGGTGGATGAAGGAGCAGACAGGTAGCATCTGCCAGTATCTG 1209
gi|16878146|gb|BC017280.1|BC01    AGGACATCCGGTGGATGAAGGAGCAGACGGGCAGCATCTGCCAGTATCTG 1342
* ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      GTGATGAGGGCCAAGAGGAAATTGGGTGACCATCTGCCTTCCAGACTGTC 1244
gi|34861241|ref|XM_341960.1|      GTGATGAGGGCCAAGAGGAAATTGGGTGACCATCTACCTTCCAGACTGTC 1259
gi|16878146|gb|BC017280.1|BC01    GTGATGCGGCCCAAGAGGAGCTGGGCAGGCACCTGCCCTCCAGGCTGCC 1392
***** * ***** ** ** ** ** ** ** ** ** ** ** ** ** ** *

gi|26327464|dbj|AK031609.1|      TGAGCAGGTGGAAGTGCAGCGTGCCTGCTCTGCTGCCACTGT 1294
gi|34861241|ref|XM_341960.1|      TGAGCAGGTGGAGCTGCGGCGTGCCTGCTCTGCTGCCACTGT 1309
gi|16878146|gb|BC017280.1|BC01    GGAGCAGGTGGAGCTGCGGCGCTGCCAGTGCCTGCTGCCACTGT 1442
***** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      CTTGCGCCACCTACAGTGAGGCCCTACCCAAGTGGGTACGAAACAACCTC 1344
gi|34861241|ref|XM_341960.1|      CTTGCGCCACCTACAGTGAGGCCCTGCCCAAGTGGGTACGAAACAACCTC 1359
gi|16878146|gb|BC017280.1|BC01    CCTGCGCGCCTACAGAGAGGCACTGCCCGGCTGGATGCGCAACAACCTC 1492
* ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      TCACTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGTACT 1394
gi|34861241|ref|XM_341960.1|      TCACTGGGGGACGCGCTGGCCAAGTGGGAAGAATGCCAGCGTCAGTACT 1409
gi|16878146|gb|BC017280.1|BC01    TCGCTGGGGGACGCGCTGGCCAAGTGGGAGGAGTGCCAGCGCCAGCTGCT 1542
** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCCGATGCCTTGCGCA 1444
gi|34861241|ref|XM_341960.1|      GCTGGGTCTCTTCTGCACCAATGTGGCCTTCCCGCCGATGCCTTGCGCA 1459
gi|16878146|gb|BC017280.1|BC01    GCTCGGCCTCTTCTGCACCAACGTGGCCTTCCCGCCGAAGCTCTGCGCA 1592
*** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      TCGCGCACCTGCCAGCCC-----CACTGCCGCAGATCCTGCCACCCCA 1488
gi|34861241|ref|XM_341960.1|      TCGCGCACCTGCCAGCCC-----CACCGCCACAGATCCTGCCACCCCA 1503
gi|16878146|gb|BC017280.1|BC01    TCGCGCACCCGCGGACCCGGCTCCCGCCCCCGCGGACCCAGCATCCCCG 1642
***** ** ***** ** ***** ** ***** ** *****

gi|26327464|dbj|AK031609.1|      CAGGATCCAC----CTGGCCTCCCGCCTTGCTGAGAATCACCATTCCCAC 1534
gi|34861241|ref|XM_341960.1|      CAGGATCCAT----CTGGCCTCCACCTTGCTGA----- 1533
gi|16878146|gb|BC017280.1|BC01    CAGCACCAGCTGGCCGGGCTGCCCTTGCTGAGCACCCTGCTCCCGA 1692
*** * * ** ***** ** *****

gi|26327464|dbj|AK031609.1|      ATCGCCCGGCTACCAGCCAAGCTCCAAGTTGTCTGCCCACTAAGAGGA 1584
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    G--GCCCCGCGGTGATCGGG-----GCCCTGGGGCTGTGAGA--- 1728

gi|26327464|dbj|AK031609.1|      GCCCCGGGGTGGAAAGATCCTGTCTGCCCCGGCTCTCCCCCTTACATG 1634
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    -CCCCGACCTCTCGAGGAACC---CTGCCTGAGACGCCTCCATTAC-CA 1773

gi|26327464|dbj|AK031609.1|      CTGTGGAATGAGGACATAGGACCCTGCACAGCTGCAAGTGGGCTTTCGAT 1684
gi|34861241|ref|XM_341960.1|      -----
gi|16878146|gb|BC017280.1|BC01    CTGCGCAGTGAGATGAGGGGACTCACAGTTGCCAAGAG-GGGTCTTTGCC 1822
```

**Figure 20. (4 of 4)**

gi 26327464 dbj AK031609.1	GTGAAACCTTTCACCAGCCACTCACTATGCTACTCCTGGTGGGGAGGGAT	1734
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	GTGGGCCCCCTCGCCAGCCACTCACCA-GCTGCATGCACTGAGAGGGGAG	1871
gi 26327464 dbj AK031609.1	GGGGAGTCGCCCTCCCCGGAGCCACAGAGCCCTCCCCCGTCACGTC--	1782
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	GTTTCACACCCCTCCCCTGGGCGCTGAGGCCCGCGCACCTGTGCCTT	1921
gi 26327464 dbj AK031609.1	ACCTGTGCCTTACTCCTGCCCACCA--CCTTTTCAGTGCAGGGTCAGTCT	1830
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	AATCTTCCCTCCCCTGTGCTGCCCGAGCACCTCCCCGCCCTTTACTCC	1971
gi 26327464 dbj AK031609.1	TAAGAACTCCACATCTGCTGCTGC-TCCCTGGTGTCCAAGTTTCCTTGCA	1879
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	TGAGAACTTTGCAGCTGCCCTTCCCTCCCGTTTTTCATGGCCTGCTGAA	2021
gi 26327464 dbj AK031609.1	GA--GTGTGTGAAGAATTATTTATTTTTCGCCAAAGCAGATCTAATAAAAG	1927
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	ATATGTGTGTGAAGAATTATTTATTTTTCGCCAAAGCACATGTAATAAATG	2071
gi 26327464 dbj AK031609.1	CCACAGCTCAGCTTCTGCCTTCTCACTTCTGCATGCT-----	1965
gi 34861241 ref XM_341960.1	-----	
gi 16878146 gb BC017280.1 BC01	CTGCAGCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2121
gi 26327464 dbj AK031609.1	-	
gi 34861241 ref XM_341960.1	-	
gi 16878146 gb BC017280.1 BC01	A	2122

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